

## Appendix B

\*\*\*\*\* [align] \*\*\*\*\*

options = -align -type=protein -matrix=blosum -gapdist=8 -maxdiv=40 -outorder=aligned -gapopen=10 -gapext=0.2 -pwmatrix=blosum -pwgapopen=10 -pwgapext=0.1

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence type explicitly set to Protein

Sequence format is Pearson

Sequence 1: E1-A0209P-2 498 aa

Sequence 2: E1-A0209P-8 459 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 34

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Delayed

Sequence:2 Score:2988

Alignment Score 779

queryaln

CLUSTAL W (1.83) multiple sequence alignment

```

E1-A0209P-2  MATVHQKNMSTLKQRKEDFTGLNGGSI TEINAVTSI ALVTYI SWNLLKNSNLMPPGISS
E1-A0209P-8  -----MSYKLEKAEFVSNLTGSSSIETCGLLLI G IACNVLWVNM TARNI LPKGN-L
               : * . * * * . * . * * . : * . : * . : * . * * *

E1-A0209P-2  VQYI I D F A L N W A L L S I T I Y A S E P Y L L N T L I L L P G L L A F I Y G K F T S S S K P S N P I Y N K K K
E1-A0209P-8  G F L V E F F I F G L I P L F V I Y V S S K V G V F T L G I A S F L P S F V L H V I S P I N W D V L R R K P G G C L T K
               : * : : . * : : . : * : : * * : : : : : : : : * * . *

E1-A0209P-2  M I T Q R F Q L E K K P Y I T A Y R G G M L I L T A I A I L A V D F P I F P R R F A K V E T W G T S L M D L G V G S F V
E1-A0209P-8  K N E N T F D R - R I A G V T F Y R S Q M L V T V T G I L A V D F T L F P R R Y A K V E T W G T S L M D L G V G S F M
               : * : : . : * * * . * : : * . * * * * . * * * * . * * * * *

E1-A0209P-2  F S N G I V S S R A L L K N L S L K S K P S F L K N A F N A L K S G G T L L F L G L L R L F F V K N L E Y G E H V T E Y
E1-A0209P-8  F S S G T V A G R -----K N D I K K P N A F K N V L W N S F I L L I L G F A R M F L T K S I N Y G E H V S E Y
               * * * * . * . * . : * . : . * * * * . * * : * . : * * * * *

E1-A0209P-2  G V H W N F F I T L S L L P L V L T F I D P V T R M V P R C S I A I F I S G I Y E W L L K D R T L N F L I L A D R N
E1-A0209P-8  G M H W N F F F T L G F M A L G V F F R R S L K K V S Y F N L A T F I T L L H H G L L V L T P - F Q K W A L S A P R T
               * * * * * . * * : : * : : : * . : * * * : : * * : : : : * .

E1-A0209P-2  C F F S A N R E G I F S F L G Y G S I F L W G Q N T G F Y L L G N K P T L N N L Y K P S T O D V V A A K S K S T W D Y
E1-A0209P-8  N I L A Q N R E G I A S L P G Y I A I Y F Y G M Y T G S V L A D R P L M Y -----T R A E S W K R
               : : : * * * * . * : * : : * * * . * : : : : : : : : : : : * .

E1-A0209P-2  W T S V T P L S G L C I W S T I F L V I S Q L V F Q Y H P Y S V S R R F A N L P Y T L W V I T Y N L L F L T G Y G L T D
E1-A0209P-8  F Q R L L F P - L G I L L V L Y L V S -----N F L S V G V S R R L A N T P Y V A N V A F I N M F F L T I Y I L I D
               : : : * * * . : : * * : : . * * * : * * * . * * : * * * * *

E1-A0209P-2  K I F G N S S E Y Y - K V A E G L E S I N S N G L F L F L L A N V S T G L V N M S M V T I D S S P L K S F L V L L A Y
E1-A0209P-8  A Y L F P S S V P Y G S R V P K L E D A N N G L L V F L I A N V L T G V V N L S F D T L H S S N A K G L T I M T M Y
               : * * * * : * : : * * . * * * : * * * * . * * : * . * * : : : *

E1-A0209P-2  C S F I A V I S V F L Y R K R I F I K L
E1-A0209P-8  L F I I G Y M A H W L A Q H G I R F R L
               : * . : : * : : : * : : *

```

query.dnd

(E1-A0209P-2:0.32789, E1-A0209P-8:0.32789);

\*\*\*\*\* [align] \*\*\*\*\*

CLUSTAL W (1.83) Multiple Sequence Alignments

query.aln  
CLUSTAL W (1.83) multiple sequence alignment

```
query.dnd
(E1-A0209P-2:0.33032,E1-A0209P-14:0.33032);
```

## Appendix B

\*\*\*\*\* [align] \*\*\*\*\*

options = -align -type=protein -matrix=blosum -gapdist=8 -maxdiv=40 -outorder=aligned -gapopen=10 -gapext=0.2 -pwmatrix=blosum -pwgapopen=10 -pwgapext=0.1

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence type explicitly set to Protein

Sequence format is Pearson

Sequence 1: E1-A0209P-8 459 aa

Sequence 2: E1-A0209P-14 598 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 33

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Delayed

Sequence:2 Score:2939

Alignment Score 741

queryaln

CLUSTAL W (1.83) multiple sequence alignment

```
E1-A0209P-8      -MSYKLEKEAFVSNLTGSSSIETCGLLIGIACHVLWVNMNTARNILPKGN-----LGFL
E1-A0209P-14      MGDYKSAKEAFVSDNPGASIWSINAVSLVALATYALWIALSPYIRHGLNNYLICVLPLL
                  ** ***** : * * . . : * : * * : : * * * * *
```

```
E1-A0209P-8      VEFFIFCLIPLFVIYVSSKVGVTLCIAS-----
E1-A0209P-14      FGVTIFSTSPLVFTSFLSIISLAFITKQKCFKSVSSPEKPKGQWLDSDSDDEEPAEPAS
                  . . ** . * . . * . : : : .
```

```
E1-A0209P-8      -----FL
E1-A0209P-14      AAGSAVSPVKLLPSQVAFASGSLSPDPTTSPMSPSSSSASGHEDPLGIMGVNRRRSL
                  : *
```

```
E1-A0209P-8      PSFVLHVISPINHDLR-----RKPGCCLTKKNENTFDRRIAGVTFYRSQMMLVTYTCI
E1-A0209P-14      EGVSLDVPSHIDSKVRISPPYLRLLKSRATKAQWVKEKGRLPFLTIVYRAHMMMLTVIGI
                  . . * * * * : * . . * * : . . * : * * : * * * * *
```

```
E1-A0209P-8      LAVDFTLFPRRYAKVETWGTSLMDLGVGSGFMFSSGTVAGRKNDIKKPNFAKN-----
E1-A0209P-14      LAVDFEVFPRWQKGCDFGTSLMDVGVSFVFSGLGVSTKSLSPPPPTPTPSSPALNSHI
                  ***** : * * : * * * * * * * * * * : : . . * . .
```

```
E1-A0209P-8      -----VLWNSFILLILGFARMFLTKSINYQEHVSEYGMHWNFFFTLGFMALG
E1-A0209P-14      IPLTPSPFTSILISLRKSIPIILVLGFIRLIMVKGSDYPEHVTEYGVHWNFFFTLALVPVL
                  * : * : * * * * : : : * : * * * : * * * * * * * * : : :
```

```
E1-A0209P-8      VFFRRSLKKVSYFNLATFITLLHHGLLVLPFGKWALSAPRTNIIAQNREGIASLPGYI
E1-A0209P-14      AVGIRPLTQWLRLWSVLGYIISLLHQLWLTYY-LQSI VFSFGRSGIFLANKEGFSSLPGYL
                  . . : * : : : * . : * * * : * : * : * * : * : * : * * * * *
```

```
E1-A0209P-8      AIYFYGMYTGSVVLADRP-----LMYTRAESWKRFQRLFPGLILLVLYLVSNFLSV
E1-A0209P-14      SIFLIGLSIGDHVLRSLPPRRERVVSETNEEHEQSHFERKKLDLIMELIGYSLGWALL
                  : : : * : * * * . . . : * * : * : * : * : * : : :
```

```
E1-A0209P-8      G-----VSRRLANTPYVANVAFINMFFLTIIYILIDAYLPSSVPYGSR---VPKLE
E1-A0209P-14      GGWIWAGGEVSRRLANAPYVFWVAAYNTTFLGYLLTHIIPSPTSQTSPSILVPPLLD
                  * ***** * * * * * * : : : . . * * * * *
```

```
E1-A0209P-8      DANNGLLVFLIANVLGVVNLSDTLHSSNAKGLTIMMYLFIICYMAHWLAQHGI RFR
E1-A0209P-14      AMNKNGLAIFLAANLLTGLVNVSMKTMYPAPAWLSMGVLMLYTLTI SCVGWILKGRRIKI-
                  * : * * : * * * * * * * : : : . . : : : * : . * : * : :
```

```
E1-A0209P-8      L
E1-A0209P-14      -
```

query.dnd

(E1-A0209P-8:0.33007, E1-A0209P-14:0.33007);